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Shifts in microbial communities with increasing soil fertility across a chronosequence of paddy cultivation in subtropical China

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ABSTRACT

An understanding of microbial community assembly and succession are keys to uncovering mechanisms underlying soil fertility development. The dynamics of microbial communities during a paddy soil chronosequence were investigated by phospholipid fatty acid profiling and amplicon high throughput sequencing. The upper 20 cm were sampled from soils after 5, 15, 30 and 100 years of paddy use and from adjacent barren land. Enzyme activities and contents of soil organic carbon, nitrogen and phosphorus of paddy fields strongly increased compared to barren land, and continued to increase at least up to 100 years of paddy cultivation. The increasing soil trophic status favored bacteria over fungi, and fast-growing copiotrophic bacteria gradually replaced slow-growing oligotrophic bacteria. The genus *Ignavibacterium* with versatile metabolism was identified as an indicator of the bacterial community in year 30 and 100. The variations of bacterial α-diversity tended to stabilize, but species richness continued to increase after 30 years of paddy use. The β-diversity indicated that bacterial community structure in paddy fields differed from that in barren land. The soils of 5 and 15 years of paddy cultivation clustered into one group separated from the group formed from the year 30 and 100. Redundancy analysis indicated that two stoichiometric ratios: C/N and C/P were the major factors affecting microbial community succession. We conclude that long-term paddy cultivation resulted in changes in biochemical properties and variations in trophic pattern of microbial communities, corresponding to increasing soil fertility.

1. Introduction

Paddy soils are anthropogenic soils (Antrosols or Technosols according to WRB 2014) and are a major resource for food production. Important pedogenic processes and transformations associated with anthropogenic activities have been identified and are well described concerning paddy soil genesis (Chen et al., 2011; Cheng et al., 2009; Kogel-Knabner et al., 2010; Wang et al., 2015). During the process of paddy cultivation, soil fertility evolution is defined as change in the ability of a soil supplying nutrients to crops (Shang et al., 2014). Soil fertility is mainly regulated by plants and microorganisms (Hartman et al., 2008), and in turn soil properties are the major factor shaping microbial communities (Cline and Zak, 2015; Cui et al., 2012; Wang et al., 2015). However, it is hard to disentangle the relationship between nutrient accumulation and microbial community succession during paddy soil development.

Most previous studies have reported the profiles of soil properties at a given stage of paddy cultivation, and this may conceal the dynamics of soil development (Su et al., 2015). Chronosequence approach provide insight into the rates and directions of soil ecosystem evolution spanning multiple time-scales due to the advantage of space-for-time substitution (Jangid et al., 2013; Jones et al., 2009). The phyla *α-Proteobacteria* and *Verrucomicrobia* are major indicators for two stages of bacterial community succession in paddy soils: a rapid-succession with clear increases in bacterial diversity within the first several decades and thereafter, a long gradual-succession stage lasting for centuries (Cui et al., 2012). Many researchers have depicted the dynamics of soil microbial community succession along chronosequence, and have

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